RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: *10/686,490A*

Source: *1FWO*

Date Processed by STIC: *8/26/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
   Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/686,490 A_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _1,2_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." **Please explain source of genetic material in <220> to <223> section.**
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 08/26/2004
PATENT APPLICATION: US/10/686,490A   TIME: 11:28:05

Input Set : A:\35991.ST25-US.txt
Output Set: N:\CRF4\08262004\J686490A.raw

```
      3 <110> APPLICANT: Bayer Aktiengesellschaft
W-->  4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
W-->  5 <130> FILE REFERENCE: LeA 35 991
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/686,490A
C-->  6 <141> CURRENT FILING DATE: 2003-10-15
W-->  6 <160> NUMBER OF SEQ ID: 2
      7 <170> SOFTWARE: PatentIn version 3.1
      9 <210> SEQ ID NO: 1
     10 <211> LENGTH: 885
     11 <212> TYPE: DNA
     12 <213> ORGANISM: artificial
W--> 13 <220> FEATURE:
     14 <221> NAME/KEY: CDS
     15 <222> LOCATION: (1)..(885)
     16 <223> OTHER INFORMATION:
W--> 18 <400> 1
     19 atg gca cag gtg aag gcc aac ggc att acc ctc gag tat gaa gag cag       48
     20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
     21 1               5                   10                  15
     23 ggc cat cgc cac cat ccg tcc atg ctc ctc att atg ggc ctg ggc ggc       96
     24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
     25              20                  25                  30
     27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga      144
     28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
     29          35                  40                  45
     31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac gcg ggg ctt tcg acg      192
     32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
     33      50                  55                  60
     35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctc ctg      240
     36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
     37 65                  70                  75                  80
     39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctc gac gac atg      288
     40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
     41              85                  90                  95
     43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc      336
     44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
     45              100                 105                 110
     47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg      384
     48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
     49          115                 120                 125
     51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc      432
     52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
     53      130                 135                 140
```

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PATENT APPLICATION: US/10/686,490A   TIME: 11:28:05

Input Set : A:\35991.ST25-US.txt
Output Set: N:\CRF4\08262004\J686490A.raw

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55 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag      480
56 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
57 145                 150                 155                 160
59 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac      528
60 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
61                     165                 170                 175
63 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag      576
64 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
65                 180                 185                 190
67 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc      624
68 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
69             195                 200                 205
71 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg      672
72 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
73     210                 215                 220
75 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg      720
76 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
77 225                 230                 235                 240
79 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac      768
80 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
81                 245                 250                 255
83 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac      816
84 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
85             260                 265                 270
87 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac      864
88 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
89             275                 280                 285
91 gcc gcg gcc gcg gaa gct taa                                          885
92 Ala Ala Ala Ala Glu Ala
93     290
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 294
98 <212> TYPE: PRT
99 <213> ORGANISM: artificial
102 <220> FEATURE:
102 <223> OTHER INFORMATION:
102 <400> 2
104 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
105 1               5                   10                  15
108 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
109             20                  25                  30
112 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
113         35                  40                  45
116 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
117     50                  55                  60
120 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
121 65                  70                  75                  80
124 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
125                 85                  90                  95
```

W--> (handwritten: "same error" circled around "artificial", <220>, <223>, <400>)

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DATE: 08/26/2004
TIME: 11:28:05

Input Set : A:\35991.ST25-US.txt
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```
128 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
129             100             105                 110
132 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
133         115             120                 125
136 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
137     130             135                 140
140 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
141 145             150                 155                 160
144 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
145             165             170                 175
148 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
149             180             185                 190
152 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
153         195             200                 205
156 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
157     210             215                 220
160 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
161 225             230                 235                 240
164 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
165             245             250                 255
168 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
169             260             265                 270
172 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
173         275             280                 285
176 Ala Ala Ala Ala Glu Ala
177     290
```